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ratio of 2x (or higher) than that observed for an unrelated probe in the particular hybridization assay indicates detection of a specific hybridization. Nucleic acids which do not hybridize to each other under stringent conditions can still be substantially identical if the polypeptides which they encode are substantially identical. This occurs, *e.g.*, when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code.

IN THE CLAIMS:

Please cancel claim 25.

Please replace claims 1, 8, 19, 20, 24, 26, and 36 with the following clean copies of the amended claims. A marked up version showing the amendments is provided in Appendix A, attached hereto.

1. (amended) An isolated or recombinant nucleic acid encoding menin, wherein said nucleic acid encodes a protein defined as follows:

(i) having a calculated molecular weight of about 67.5 kDa; and

(ii) (a) specifically binding to a specific polyclonal antibody raised against a protein with a sequence as set forth in SEQ ID NO:2; or

(b) having at least 60% amino acid sequence identity to a protein with a sequence as set forth in SEQ ID NO:2.

8. (amended) The isolated or recombinant nucleic acid of claim 1, wherein the nucleic acid sequence specifically hybridizes to SEQ ID NO:1 under stringent hybridization conditions comprising 50% formamide at 42°C and wash conditions comprising 0.2XSSC at 65°C for 15 minutes.

19. (amended) A method for detecting in a test sample the presence or absence of a mutation in a nucleotide sequence essentially encoding human menin or the presence or absence of a MEN1 allele comprising;

a) contacting said test sample suspected of missing a MEN1 allele or encoding a mutant form of the human menin with a first oligonucleotide having a sequence that discriminates between the wild type gene and the missing allele or mutant form, wherein the first oligonucleotide specifically hybridizes to a nucleic acid sequence comprising at least 95% identity to SEQ ID NO:3; and,

b) detecting the formation of a duplex between the gene and the first oligonucleotide sequence.

20. (amended) A method of claim 19, wherein the first oligonucleotide is unable to bind to the wild-type MEN1 gene under hybridization conditions in which the first oligonucleotide binds to the mutant sequence of MEN1.

24. (amended) A kit for detecting in a test sample the presence or absence of a mutation in a nucleotide sequence encoding a menin polypeptide, the kit comprising;

a) a container holding a first oligonucleotide sequence that discriminates between the wild type gene and the mutant form, and that specifically hybridizes to a nucleic acid sequence comprising at least 95% identity to SEQ ID NO:3; and

b) a container holding a reagent for detecting the formation of a duplex between the gene and the first nucleotide sequence.

26. (amended) The kit of claim 24, further comprising amplification primer pairs specifically binding to a human genomic DNA sequence encoding menin.

36. (amended) An expression cassette comprising a nucleic acid encoding a menin polypeptide, wherein the nucleic acid is operably linked to a promoter.